OIPE

RAW SEQUENCE LISTING   DATE: 10/29/2001
PATENT APPLICATION: US/09/975,308   TIME: 16:00:15

        Input Set : A:\LEX-0252-USA SEQLIST.TXT
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 4 <110> APPLICANT: Friddle, Carl Johan
 5        Hilbun, Erin
 6        Gerhardt, Brenda
 7        Mathur, Brian
 8        Walke, D. Wade
 9        Turner, C. Alexander Jr.
11 <120> TITLE OF INVENTION: Novel Human 7TM Proteins and Polynucleotides Encoding the
Same
14 <130> FILE REFERENCE: LEX-0252-USA
16 <140> CURRENT APPLICATION NUMBER: US/09/975,308
16 <141> CURRENT FILING DATE: 2001-10-11
16 <150> PRIOR APPLICATION NUMBER: US 60/239,592
17 <151> PRIOR FILING DATE: 2000-10-11
19 <160> NUMBER OF SEQ ID NOS: 20
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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25 <212> TYPE: DNA
26 <213> ORGANISM: homo sapiens
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31 atgggtcgag gaaacagcac tgaagtgact gaattccatc ttctgggatt tggtgtccaa 180
32 cacgaatttc agcatgtcct tttcattgta cttcttctta tctatgtgac ctccctgata 240
33 ggaaatattg gaatgatctt actcatcaag accgattcca gacttcaaac acccatgtac 300
34 ttttttccac aacatttggc ttttgttgat atctgttata cttctgctat cactcccaag 360
35 atgctccaaa gcttcacaga agaaaataat ttgataacat ttcggggctg tgtgatacaa 420
36 ttcttagttt atgcaacatt tgcaaccagt gactgttacc tcctagctat tatggcaatg 480
37 gattgttatg ttgccatctg taagcccctt cgctatccca tgatcatgtc ccaaacagtc 540
38 tacatccaac tcgtagctgg ctcatatatt ataggctcaa taaatgcctc tgtacataca 600
39 ggttttacat tttcactgtc cttctgcaag tctaataaaa tcaatcactt tttctgtgat 660
40 ggtctcccaa ttcttgccct ttcatgctcc aacattgaca tcaacatcat tctagatgtt 720
41 gtctttgtgg gatttgactt gatgttcact gagttggtca tcatcttttc ctacatctac 780
42 attatggtca ccatcctgaa gatgtcttct actgctggga ggaaaaaatc cttctccaca 840
43 tgtgcctccc acctgacagc agtaaccatt ttctatggga cactctctta catgtactta 900
44 cagcctcagt ctaataattc tcaggagaat atgaaagtag cctctatatt ttatggcact 960
45 gttattccca tgttgaatcc tttaatctat agcttgagaa ataaggaagg aaaataa    1017
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48 <211> LENGTH: 338
49 <212> TYPE: PRT
50 <213> ORGANISM: homo sapiens
52 <400> SEQUENCE: 2
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55 Leu Gln Lys Val Thr Arg Met Phe Leu Leu Phe Trp Val Leu Leu Leu
56             20                  25                  30
57 Val Leu Ser Arg Leu Leu Val Val Met Gly Arg Gly Asn Ser Thr Glu
58             35                  40                  45
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60      50                  55                  60
61 His Val Leu Phe Ile Val Leu Leu Leu Ile Tyr Val Thr Ser Leu Ile
62 65                  70                  75                  80
63 Gly Asn Ile Gly Met Ile Leu Leu Ile Lys Thr Asp Ser Arg Leu Gln
64              85                  90                  95
65 Thr Pro Met Tyr Phe Phe Pro Gln His Leu Ala Phe Val Asp Ile Cys
66              100                 105                 110
67 Tyr Thr Ser Ala Ile Thr Pro Lys Met Leu Gln Ser Phe Thr Glu Glu
68          115                 120                 125
69 Asn Asn Leu Ile Thr Phe Arg Gly Cys Val Ile Gln Phe Leu Val Tyr
70      130                 135                 140
71 Ala Thr Phe Ala Thr Ser Asp Cys Tyr Leu Leu Ala Ile Met Ala Met
72 145                 150                 155                 160
73 Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Arg Tyr Pro Met Ile Met
74              165                 170                 175
75 Ser Gln Thr Val Tyr Ile Gln Leu Val Ala Gly Ser Tyr Ile Ile Gly
76              180                 185                 190
77 Ser Ile Asn Ala Ser Val His Thr Gly Phe Thr Phe Ser Leu Ser Phe
78              195                 200                 205
79 Cys Lys Ser Asn Lys Ile Asn His Phe Phe Cys Asp Gly Leu Pro Ile
80      210                 215                 220
81 Leu Ala Leu Ser Cys Ser Asn Ile Asp Ile Asn Ile Ile Leu Asp Val
82 225                 230                 235                 240
83 Val Phe Val Gly Phe Asp Leu Met Phe Thr Glu Leu Val Ile Ile Phe
84              245                 250                 255
85 Ser Tyr Ile Tyr Ile Met Val Thr Ile Leu Lys Met Ser Ser Thr Ala
86              260                 265                 270
87 Gly Arg Lys Lys Ser Phe Ser Thr Cys Ala Ser His Leu Thr Ala Val
88          275                 280                 285
89 Thr Ile Phe Tyr Gly Thr Leu Ser Tyr Met Tyr Leu Gln Pro Gln Ser
90      290                 295                 300
91 Asn Asn Ser Gln Glu Asn Met Lys Val Ala Ser Ile Phe Tyr Gly Thr
92 305                 310                 315                 320
93 Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu
94              325                 330                 335
95 Gly Lys
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100 <211> LENGTH: 897
101 <212> TYPE: DNA
102 <213> ORGANISM: homo sapiens
104 <400> SEQUENCE: 3
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106 cacgaatttc agcatgtcct tttcattgta cttcttctta tctatgtgac ctccctgata 120
107 ggaaatattg gaatgatctt actcatcaag accgattcca gacttcaaac acccatgtac 180
108 ttttttccac aacatttggc ttttgttgat atctgttata cttctgctat cactcccaag 240
109 atgctccaaa gcttcacaga agaaaataat ttgataacat tcgggggctg tgtgatacaa 300
110 ttcttagttt atgcaacatt tgcaaccagt gactgttacc tcctagctat tatggcaatg 360
111 gattgttatg ttgccatctg taagcccctt cgctatccca tgatcatgtc ccaaacagtc 420
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113 ggtttacat tttcactgtc cttctgcaag tctaataaaa tcaatcactt tttctgtgat 540
114 ggtctcccaa ttcttgccct ttcatgctcc aacattgaca tcaacatcat tctagatgtt 600
115 gtctttgtgg gatttgactt gatgttcact gagttggtca tcatcttttc ctacatctac 660
116 attatggtca ccatcctgaa gatgtcttct actgctggga ggaaaaaatc cttctccaca 720
117 tgtgcctccc acctgacagc agtaaccatt ttctatggga cactctctta catgtactta 780
118 cagcctcagt ctaataattc tcaggagaat atgaaagtag cctctatatt ttatggcact 840
119 gttattccca tgttgaatcc tttaatctat agcttgagaa ataaggaagg aaaataa    897
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 298
123 <212> TYPE: PRT
124 <213> ORGANISM: homo sapiens
126 <400> SEQUENCE: 4
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129 Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
130              20                  25                  30
131 Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
132          35                  40                  45
133 Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
134      50                  55                  60
135 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
136 65                  70                  75                  80
137 Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
138              85                  90                  95
139 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
140              100                 105                 110
141 Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
142          115                 120                 125
143 Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
144      130                 135                 140
145 Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
146 145                 150                 155                 160
147 Gly Phe Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Lys Ile Asn His
148              165                 170                 175
149 Phe Phe Cys Asp Gly Leu Pro Ile Leu Ala Leu Ser Cys Ser Asn Ile
150              180                 185                 190
151 Asp Ile Asn Ile Ile Leu Asp Val Val Phe Val Gly Phe Asp Leu Met
152          195                 200                 205
153 Phe Thr Glu Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met Val Thr
154      210                 215                 220
155 Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Ser Phe Ser Thr
156 225                 230                 235                 240
157 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
158              245                 250                 255
159 Tyr Met Tyr Leu Gln Pro Gln Ser Asn Asn Ser Gln Glu Asn Met Lys
160              260                 265                 270
161 Val Ala Ser Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
162          275                 280                 285
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Input Set : A:\LEX-0252-USA SEQLIST.TXT
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174 cgaggaaaca gcactgaagt gactgaattc catcttctgg gatttggtgt ccaacacgaa 120
175 tttcagcatg tccttttcat tgtacttctt cttatctatg tgacctccct gataggaaat 180
176 attggaatga tcttactcat caagaccgat tccagacttc aaacacccat gtactttttt 240
177 ccacaacatt tggcttttgt tgatatctgt tatacttctg ctatcactcc caagatgctc 300
178 caaagcttca cagaagaaaa taatttgata acatttcggg gctgtgtgat acaattctta 360
179 gtttatgcaa catttgcaac cagtgactgt tacctcctag ctattatggc aatggattgt 420
180 tatgttgcca tctgtaagcc ccttcgctat cccatgatca tgtcccaaac agtctacatc 480
181 caactcgtag ctggctcata tattataggc tcaataaatg cctctgtaca tacaggtttt 540
182 acattttcac tgtccttctg caagtctaat aaaatcaatc acttttttctg tgatggtctc 600
183 ccaattcttg ccctttcatg ctccaacatt gacatcaaca tcattctaga tgttgtcttt 660
184 gtgggatttg acttgatgtt cactgagttg gtcatcatct tttcctacat ctacattatg 720
185 gtcaccatcc tgaagatgtc ttctactgct gggaggaaaa aatccttctc cacatgtgcc 780
186 tcccacctga cagcagtaac cattttctat gggacactct cttacatgta cttacagcct 840
187 cagtctaata attctcagga gaatatgaaa gtagcctcta tattttatgg cactgttatt 900
188 cccatgttga atcctttaat ctatagcttg agaaataagg aaggaaaata a      951
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191 <211> LENGTH: 316
192 <212> TYPE: PRT
193 <213> ORGANISM: homo sapiens
195 <400> SEQUENCE: 6
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199             20                  25                  30
200 Leu Gly Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val
201         35                  40                  45
202 Leu Leu Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile
203     50                  55                  60
204 Leu Leu Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe
205 65                  70                  75                  80
206 Pro Gln His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr
207             85                  90                  95
208 Pro Lys Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe
209             100                 105                 110
210 Arg Gly Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser
211         115                 120                 125
212 Asp Cys Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile
213     130                 135                 140
214 Cys Lys Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile
215 145                 150                 155                 160
216 Gln Leu Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val
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217                 165                 170                 175
218 His Thr Gly Phe Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Lys Ile
219                 180                 185                 190
220 Asn His Phe Phe Cys Asp Gly Leu Pro Ile Leu Ala Leu Ser Cys Ser
221             195                 200                 205
222 Asn Ile Asp Ile Asn Ile Ile Leu Asp Val Val Phe Val Gly Phe Asp
223     210                 215                 220
224 Leu Met Phe Thr Glu Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met
225 225                 230                 235                 240
226 Val Thr Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Ser Phe
227             245                 250                 255
228 Ser Thr Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr
229             260                 265                 270
230 Leu Ser Tyr Met Tyr Leu Gln Pro Gln Ser Asn Asn Ser Gln Glu Asn
231             275                 280                 285
232 Met Lys Val Ala Ser Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn
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235 305                 310                 315
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240 <212> TYPE: DNA
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246 cctagatgga agttgcattt taagaatact agtacaaaga cactttgaag ccttcaaaaa 180
247 tatgtgaata tgaacatatt ttgggaaatt gctctccaat taattctact aatttcaaga 240
248 actagaaaga gaaataaaat aagtggctgt gaataattat gtttctaaaa aggtacagaa 300
249 ttacatttta acgttattta gaataaatac aaatacctgt ttaatatagt gaaaaaatgc 360
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253 attgaaaaaa gtgacttaaa atatagagcc attttattgc aaaaagtcac aaggatgttc 600
254 ctgcttttct gggtccttct cttggtcctt tctagacttt tggtagtcat gggtcgagga 660
255 aacagcactg aagtgactga attccatctt ctgggatttg gtgtccaaca cgaatttcag 720
256 catgtccttt tcattgtact tcttcttatc tatgtgacct ccctgatagg aaatattgga 780
257 atgatcttac tcatcaagac cgattccaga cttcaaacac ccatgtactt ttttccacaa 840
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263 tcactgtcct tctgcaagtc taataaaatc aatcactttt tctgtgatgg tctcccaatt 1200
264 cttgcccttt catgctccaa cattgacatc aacatcattc tagatgttgt ctttgtggga 1260
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267 ctgacagcag taaccatttt ctatgggaca ctctcttaca tgtacttaca gcctcagtct 1440
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VERIFICATION SUMMARY   DATE: 10/29/2001
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Input Set : **A:\LEX-0252-USA SEQLIST.TXT**
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date